

**A single nucleotide polymorphism in the 5' UTR of ovine FASN gene is associated with milk fat yield***A. Sanz<sup>1</sup>, C. Serrano<sup>1</sup>, J.H. Calvo<sup>2</sup>, P. Zaragoza<sup>1</sup>, J. Altarriba<sup>3</sup> and C. Rodellar<sup>1</sup>*

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Fatty acid synthase (FASN) is a complex homodimeric enzyme that regulates de novo biosynthesis of long-chain fatty acids. Ovine FASN gene maps on OAR11, where a QTL affecting the fatty acid composition of milk sheep has been identified. Besides, some SNPs in the bovine FASN gene have been also associated with milk-fat content and with fatty acid composition of milk and beef. Hence, it is a candidate gene for fat content in milk animals. In this study we screened the 5' untranslated region of the ovine FASN gene, and we identified a G>A substitution in the untranslated exon 1 (g.982G>A) according to the bovine FASN genomic sequence (AF285607). The SNP was tested in Assaf individuals grouped for milk fat production, including 50 animals with the highest milk-fat content and 50 animals with the lowest milk-fat content. Allele frequencies differed significantly ( $P=0.0121$ ) between fat content groups. Since the mammalian FASN gene is regulated at both the transcriptional and post-transcriptional levels; this polymorphism could modify the putative Sp1, Sp2, Sp3 and Sp4 transcription factors binding site in the untranslated exon 1 and also could alter FASN mRNA stability. The prediction of RNA secondary structure within the 5'UTR predicts that allele G may produce a more stable folding of the 5'UTR because it has a lower free energy (-43.0 kcal/mole) with respect to allele A (-36.9 kcal/mole). Those evidences suggest the implication of this polymorphism in the variation in milk-fat content in sheep. We propose that the ovine FASN gene is a candidate gene for a milk-fat content QTL.